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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/446,024	12/16/1999	FREDERIC BESEME	105045	1689

7590   01/31/2002

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EXAMINER
LEFFERS JR, GERALD G

ART UNIT	PAPER NUMBER
1636	14

DATE MAILED: 01/31/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 07-01)

	Application No.		Applicant(s)
Office Action Summary	09/446,024		BESEME ET AL.
	Examiner		Art Unit
	Gerald G Leffers Jr.		1636

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on <u>09 November 2001</u> .

2a)☐ This action is **FINAL**.   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) <u>1-14 and 18-38</u> is/are pending in the application.

    4a) Of the above claim(s) <u>13,14 and 37</u> is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) <u>1-12,18-36 and 38</u> is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

    If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All b)☐ Some * c)☒ None of:

      1.☒ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____ .

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

    a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)	4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)	5) ☐ Notice of Informal Patent Application (PTO-152)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) <u>4, 5</u> .	6) ☐ Other: .

DETAILED ACTION

Receipt is acknowledged of applicants' preliminary amendment, filed 5/29/01 as Paper

No. 9, in which several claims were amended (claims 1-4, 7-14, 18-20) and new claims added

(claims 21-38).

Receipt is also acknowledged of applicants' preliminary amendment, filed 11/9/01 as

Paper No. 12, in which the specification was amended to include sequence identifiers and in

which a new paper copy of the sequence listing, computer readable form and corresponding

attorney's statement were submitted.

Election/Restrictions

Applicant's election with traverse of Group I (claims 1-12, 15-20, 21-36, 38), claims

drawn toward nucleic acids of a human endogenous retroviral genome and methods of using the

same for diagnosis, in Paper No. 9 is acknowledged. The traversal is on the ground(s) that the

therapeutic composition of claim 20 has a common technical feature (i.e. nucleic acid sequence)

with the nucleic acids and methods of Group I. This is not found persuasive because it is not

necessarily true that the nucleic acids used in the methods of Group I will be found in the

therapeutic composition of claim 20. Moreover, the therapeutic composition has technical

features in addition to just the presence of a nucleic acid derived from a particular source (e.g.

pharmaceutically acceptable carriers, synergistic compounds, etc.).

The requirement is still deemed proper and is therefore made FINAL.

Claims 1-14 and 18-38 are pending in this application, with claims 13-14 and 37

withdrawn from consideration as being drawn towards a nonelected invention.

Specification

This application does not contain an abstract of the disclosure as required by 37

CFR 1.72(b). An abstract on a separate sheet is required.

Claim Objections

Claims1-12, 18-36 and 38 are objected to because of the following informalities: many

of these claims lack an article (e.g. The, A, etc.) at the beginning of the claim and are

grammatically incorrect. Appropriate correction is required.

Claims 33-35 are objected to because of the following informalities: elements a), b), c)

recited in the body of these claims are not completely enclosed by parentheses, making it

somewhat unclear as to what parts of the dependent claim these elements correspond. It would

be remedial to amend the claims to enclose the recited elements completely in parentheses.

Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or
> any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and
> requirements of this title.

Claims 11 and 28-30 are rejected under 35 U.S.C. 101 because the claimed invention is

not supported by either a specific and substantial asserted utility or a well-established utility.

Each of these claims appear to be limited to nucleic acid sequences for which there

appears to be no prior art describing a nucleic acid comprising the exact same sequence and for

which a specific and substantial utility has been demonstrated. Therefore, for these sequences there appears to be no well-established utility. Moreover, the prior art does not appear to provide support for any of the asserted utilities for the claimed nucleic acids.

The specification teaches that the claimed sequences were obtained from cDNAs isolated from placenta or from a deduced genomic RNA sequence based upon alignment of several overlapping cDNAs (termed by applicants as HERV-W). This proposed genomic RNA sequence (SEQ ID NO: 11) is described as having several of the characteristics of retroviral genomic RNAs. There is no description of a single genomic clone comprising all of the deduced RNA sequences. It is unclear whether there exists in the human genome a single complete copy of the deduced RNA genome. Several elements of the deduced RNA sequence do appear to be expressed in placental cells and not in several other cell types. The specification teaches that the genomic distribution of the HERV-W sequences throughout the genome is complex, with hundreds of partial sequences scattered across several different chromosomes.

Asserted utilities for the claimed nucleic acids are several, including for example, use of the nucleic acid sequences as markers or probes for several diseases or disorders such as autoimmune disease or unsuccessful pregnancy. All of the asserted utilities are dependent upon the recited sequences actually being correlated with a particular disease or condition. However, the specification provides no convincing evidence that such specific (i.e. correlating to a specific condition) or substantial (i.e. not requiring additional experimentation to identify or confirm) utilities exist for the claimed nucleic acids. For example, the specification bases several of its asserted utilities upon the observation that other human endogenous retroviral nucleic acid sequences have some unspecified degree of correlation to disease or disorders. There is no

significant correlation, however, between the prior art endogenous retroviral sequences and the

instant nucleic acids with regard to specific diseases or disorders, and the specification provides

no convincing rational as to why one of skill in the art would expect the claimed nucleic acid

sequences to be correlated to the same conditions or diseases as is exhibited by other non-related

HERV elements. The specification also asserts that the claimed nucleic acids can be used to

diagnose risk of a pathological pregnancy or risk of unsuccessful pregnancy based upon the

observation that a few of the sequences comprised within the proposed HERV-W sequence are

expressed somewhat specifically in the placenta. However, there is no convincing rational

presented in the specification as to why the recited sequences should be associated with a

problem pregnancy. For example, there is no comparison of expression of the nucleic acids of

the invention in abnormal pregnancies to expression of the same sequences in normal

pregnancies.

Given that there is no well-established utility for nucleic acids comprising the recited

nucleotide sequences, and that there is no convincing support provided by the specification or

prior art for any of the asserted utilities such that the asserted utilities can be considered specific

and substantial, one of skill in the art would reasonably conclude that the recited nucleic acid

sequences lack specific and substantial utility.

Claims 11 and 28-30 are also rejected under 35 U.S.C. 112, first paragraph. Specifically,

since the claimed invention is not supported by either a specific and substantial asserted utility or

a well established utility for the reasons set forth above, one skilled in the art clearly would not

know how to use the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-12, 15-20, 21-36, 38 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1-4 are vague and indefinite in that the metes and bounds of the phrase "nucleic material of the retroviral genomic type" are unclear. The phrase does not appear to be well defined by the specification. For example, how homologous to a reference retroviral nucleotide sequence does a given sequence have to be in order to qualify as a nucleic acid of the "retroviral type"? How much of a nucleic acid derived from a retroviral genome must be present in order for it to be of a "retroviral genomic type"? It would be remedial to amend the claim language to more clearly indicate what is intended by the recited limitation of "nucleic material of the retroviral genomic type".

Claims 1 and 7 are vague and indefinite in that the metes and bounds of the term "equivalent" when applied to a nucleic acid sequence are unclear. The concept of equivalent protein or nucleic acid sequences does not appear to be well defined in the specification. For example, how homologous to a given reference sequence does a sequence have to be in order to qualify as an "equivalent" sequence to the reference? How much functional similarity for an encoded polypeptide to a reference polypeptide must there be in order for the nucleic or amino acid sequences to qualify as "equivalent"? It would be remedial to amend the claim language to explicitly define what is intended by the term "equivalent".

Claim 1 is also vague and indefinite in that it is unclear what is intended by the term "reference nucleotide sequence". This term does not appear to be well defined in the specification. It would be remedial to amend the claim language to clearly indicate what is intended by the recited term.

Claim 2 is vague and indefinite in that the metes and bounds of the phrase "capable of being encoded by at least a functional part of a reference nucleotide sequence" are unclear. Under what conditions is the peptide to be "capable of" being encoded by the recited sequences? Also, what exactly constitutes a "functional part" of a reference sequence? This term does not appear to be clearly defined in the specification.

Claims 3, 12 and 27 are vague and indefinite in that the metes and bounds of the term "fragment" are unclear in light of the claimed invention. What are the limits of a nucleic acid "fragment" in context of the claims? Would a single nucleic acid inserted, as specified in claims 3 and 27, between an LTR and gag gene constitute a "fragment"? From what source is the fragment to be derived? It would be remedial to amend the claim language to clearly indicate what is intended by the recited phrase.

Claim 7 is vague and indefinite in that the metes and bounds of the phrase "partial and complete" are unclear. For example, what constitutes a "complete" nucleic acid sequence according to claim 1? What constitutes a "partial" nucleic acid sequence of one of the recited clones? Would a single nucleotide satisfy this limitation?

Claim 8 is vague and indefinite in that the metes and bounds of the phrase "capable of hybridizing specifically" are unclear? Under what conditions is the hybridization to be

performed? How specific is "specific hybridization"? It would be remedial to amend the claim

to include the hybridization conditions and the limits of "specific hybridization".

Claim 9 is vague and indefinite in that it is not clear what exactly constitutes a "marker"

in the context of the claim. Does the term refer to a genetic marker or to some sort of label

attached to the probe? Upon reading the specification, it appears the term is intended to specify

some sort of label. It would be remedial to amend the claim language accordingly.

Claim 10 is vague and indefinite in that the metes and bounds of the phrase "capable of

hybridizing" are unclear? Under what conditions is the hybridization to be performed? It would

be remedial to amend the claim to include the hybridization conditions.

Claim 12 is vague and indefinite in that there is no clear and positive prior antecedent

basis for the term "nucleotide fragment" in claim 7, upon which claim 12 is dependent.

Claim 18 is vague and indefinite in that the metes and bounds of the term "and/or" are

inherently indefinite, making it unclear as to which combinations of limitations are acceptable.

Claim 20 is vague and indefinite in that the claim is drawn towards a non-elected

embodiment (i.e. a therapeutic composition). It would be remedial to amend the claim language

to delete this limitation.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the

basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) do not apply to the examination of this application as the application being examined was not (1) filed on or after November 29, 2000, or (2) voluntarily published under 35 U.S.C. 122(b). Therefore, this application is examined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

Claims 1-10, 12, 18-36 and 38 are rejected under 35 U.S.C. 102(e) as being anticipated by Perron et al (U.S. Patent No. 6,001,987; see the entire document).

The Perron et al patent teaches the identification of sequences derived from a human endogenous retroviral genome and co-infective agent (MSVR-1 and MSVR-2, respectively) and which are associated with multiple sclerosis (MS), a disease with an autoimmune component (e.g. Abstract; column 3, lines 5-30; column 4, lines 15-50). The specification of the '987 patent teaches that the nucleic acids of the invention can be used for detection of a pathogenic and/or infective agent associated with MS (e.g. column 5, lines 10-29). The specification of the '987 patent teaches examples wherein specific MSRV-1 or MSRV-2 sequences are detected in samples (e.g. plasma or blood) obtained from patients having MS (e.g. Example 6).

The attached Sequence Identity search demonstrates that the sequence described by SEQ ID NO: 11 of the instant specification has 78.4% similarity to SEQ ID NO: 57 of the '987 patent. SEQ ID NO: 11 also has 88% similarity to SEQ ID NO: 89 of the '987 patent and 86.4% similarity to SEQ ID NO: 61 of the '987 patent. Figure 1 of the instant specification teaches that

SEQ ID NOS: 1-5, 7-10 are comprised within the proposed genomic RNA sequence described

by SEQ ID NO: 11. The search report demonstrates several sequences which have very high

identity with SEQ ID NO: 11. For example, from nt 2317 to nt 2438 of SEQ ID NO: 89 of the

'987 patent, approximately 100 contiguous monomers, there is ~95% identity to SEQ ID NO: 11

of the instant specification.

Claims 1-9, 11-12, 24-27 and 31-36 are rejected under 35 U.S.C. 102(b) as being

anticipated by Pauly or Waterston (Search Report #1, result # 3, Accession No. AC000064;

available to the public since 13 November 1996).

As shown in the attached search report, Pauly and Waterston submitted the sequence of a

human BAC clone, RG083M05. This sequence was available to the public as of 13 November

1996. Applicants admit in their specification that this genomic clone was available in the art at

the time of applicants' invention and that the putative genomic RNA sequence has ~96% identity

over its length with the sequence of RG083M05 (e.g. Example 2). The entire nucleotide

sequence of RG083M05 can be used as a probe capable of hybridizing to SEQ ID NO: 11.

Nucleic acid sequences within the BAC clone can be considered as "markers" for detection.

Conclusion

Claims 1-14, 18-38 are pending. Claims 13-14 and 37 are withdrawn from consideration

as being directed towards a nonelected invention. No claims are allowed.
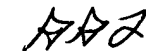
Any inquiry concerning this communication or earlier communications from the

examiner should be directed to Gerald G Leffers Jr. whose telephone number is (703) 308-6232.
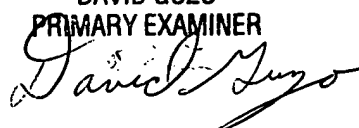
The examiner can normally be reached on 9:30am-6:00pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's

supervisor, Remy Yucel can be reached on (703) 305-1998. The fax phone numbers for the

organization where this application or proceeding is assigned are (703) 305-7939 for regular

communications and (703) 305-7939 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding

should be directed to the receptionist whose telephone number is (703) 308-0196.

Gerald G Leffers Jr.
Examiner
Art Unit 1636

ggl
January 28, 2002

DAVID GUZO
PRIMARY EXAMINER

L Number	Hits	Search Text	DB	Time stamp
1	25	beseme-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:11
7	53	blond-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:11
13	203	bouton-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
19	119	mandrand-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
25	323	mallet-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
31	618	perron-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
37	1	beseme-$.in. and blond-$.in. and bouton-$.in. and mandrand-$.in. and mallet-$.in. and perron-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:12
43	1245	beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:13
49	0	(beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.) and (herv-w)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:13
55	27	(beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.) and ((herv-$2) or (endogenous adj4 retrovir$4))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:19
61	323	((herv-$2) or (endogenous adj4 retrovir$4))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:19
67	30	((herv-$2) or (endogenous adj4 retrovir$4)).ti.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:19
73	11	((herv-$2) or (endogenous adj4 retrovir$4)).clm.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:20
79	39	(((herv-$2) or (endogenous adj4 retrovir$4)).ti.) or (((herv-$2) or (endogenous adj4 retrovir$4)).clm.)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:20
85	35	((((herv-$2) or (endogenous adj4 retrovir$4)).ti.) or (((herv-$2) or (endogenous adj4 retrovir$4)).clm.)) not ((beseme-$.in. or blond-$.in. or bouton-$.in. or mandrand-$.in. or mallet-$.in. or perron-$.in.) and ((herv-$2) or (endogenous adj4 retrovir$4)))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/01/28 08:20

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(FILE 'HOME' ENTERED AT 08:47:47 ON 28 JAN 2002)

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L3        455 S (MANDRAND, ?)/IN,AU
L4       5300 S (MALLET, ?)/IN,AU
L5       1773 S (PERRON, ?)/IN,AU
L6          8 S L1 AND L2 AND L3 AND L4 AND L5
L7          2 DUPLICATE REMOVE L6 (6 DUPLICATES REMOVED)
L8       8268 S L1 OR L2 OR L3 OR L4 OR L5
L9         40 S L8 AND HERV-W
L10        14 DUPLICATE REMOVE L9 (26 DUPLICATES REMOVED)
L11        13 S L10 NOT L6
L12         3 S L8 AND HERV-H
L13         1 DUPLICATE REMOVE L12 (2 DUPLICATES REMOVED)
L14      3520 S HUMAN (S) ENDOGENOUS (S) RETROVIR?
L15      3497 S L14 NOT (L6 OR L9 OR L12)
L16       260 S L15 AND (PLACENTA OR PREGN?)
L17         8 S L16 AND HERV-H
L18         2 DUPLICATE REMOVE L17 (6 DUPLICATES REMOVED)
L19        14 S L16 AND HERV-W
L20         5 DUPLICATE REMOVE L19 (9 DUPLICATES REMOVED)
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Access DB# 48622

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Gerald G Leffers Jr   Examiner #: 77472   Date: 8-8-01

Art Unit: 1636   Phone Number 308-6232   Serial Number: 09/446,024

Mail Box and Bldg/Room Location   Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID #11-15

— Some Claims to any 100 contiguous NT's

from Seq ID #11-15

Point of Contact:
Susan Hanley
Technical Info. Specialist
CM1 12C14 Tel: 305-4053

J approve

nuc 11-15

nuc. 11-15

41

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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: Hanley	NA Sequence (#) 5	STN
Searcher Phone #:	AA Sequence (#)	Dialog
Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up: 8/10	Bibliographic	Dr.Link
Date Completed: 8/16	Litigation	Lexis/Nexis
Searcher Prep & Review Time: 8/10	Fulltext	Sequence Systems
Clerical Prep Time:	Patent Family	WWW/Internet
Online Time: 1.5	Other	Other (specify)

PTO-1590 (1-2000)

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2001, 11:11:46 ; Search time 20850.3 Seconds
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Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Post-processing: Minimum Match 0%
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 67: gb_htg8:*
 68: gb_htg9:*
 69: gb_htg10:*
 70: gb_htg11:*
 71: gb_htg12:*
 72: gb_htg13:*
 73: gb_htg14:*
 74: gb_htg15:*
 75: gb_htg16:*
 76: gb_htg17:*
 77: gb_htg18:*
 78: gb_htg19:*
 79: gb_htg20:*
 80: gb_htg21:*
 81: gb_htg22:*
 82: gb_htg23:*
 83: gb_htg24:*
 84: gb_htg25:*
 85: gb_pr1:*
 86: gb_pr2:*
 87: gb_pr3:*
 88: gb_pr4:*
 89: gb_pr5:*
 90: gb_pr6:*
 91: gb_pr7:*
 92: gb_pr8:*
 93: gb_pr9:*
 94: gb_ro1:*
 95: gb_ro2:*
 96: gb_in4:*
 97: gb_pr10:*
 98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7489.6	98.8	7582	9	AX000966	AX000966 Sequence
2	7489.6	98.8	7582	9	AX027480	AX027480 Sequence
3	6448	85.0	56093	93	HSAC000064	AC000064 Human BAC
c 4	6448	85.0	149194	86	AC007566	AC007566 Homo sapi
c 5	6436	84.9	10499	9	AX007980	AX007980 Sequence
c 6	5824.2	76.8	158053	65	AC018926	AC018926 Homo sapi
c 7	5492	72.4	193159	61	AC009727	AC009727 Homo sapi
8	4302.2	56.7	114621	85	AC005187	AC005187 Homo sapi

```
Qy  6241 ggacctcttgttcccaaatstggaaataaccataacccataccctcaaccctcaacctgtgtaaaattt 6300
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Db  6241 GGACCTCTTGTTCCAATSTGGAAATAACCATAACCCATACCCTCAAACCTCACCTGTGTAAAATTT 6300

Qy  6301 agcaatactacacacaacaaccatccccacactcctccccacacaa 6360
         |||||||||||||||||||||||||||||||||||||||||||
Db  6301 AGCAATACTACACATACACAACCAACTCACCTGGTAACTCCCCACACAA 6360

Qy  6361 atagtctgctcacccctccaggaatattttttgtctgtsgttacctcagccatatcgttcgttg 6420
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6361 ATAGTCTGCTCACCCTCCAGGAATATTTTTTGTCTGTSGTTACCTCAGCCATATCGTTTGTTTG 6420

Qy  6421 aatggctcttcagaatctatgtgtctcattcattcttagtctgtgcccatctac 6480
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Db  6421 AATGGCTCTTCAGRAATCTARGTGTCTCCATTCATTCTTAGTGCCCCATAICTAC 6480

Qy  6481 actggaacaagaattataacagtttatgtcatatctaagcccccgcaacaaaagtaccat 6540
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Db  6481 ACTGGAACAAGAATTTAATACAGTTAITGTCATATCTAAGCCCCGCAACAAAAGTACCCATT 6540

Qy  6541 ctccttttgttataggaggaggagtgcactaggtactggcattggggttatc 6600
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Qy  6601 acaacctctactcaagttctactacaaactatctcaagaactaaatggggacatgggaacgg 6660
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Db  6601 ACAACCTCTACTCAGTTCTACTACAARACTATCTCAAGAAACTAAAAGTGGGGACATGGGAACGG 6660

Qy  6661 gtcgcgcaactccctggtcaccttgcaagatcaaacttaacccctagcagtcagtccctt 6720
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Db  6661 GTCCCGCGACTCCCCRGGTCACCTTGCCAAGATCAAACTTAACCCCTAGCCAGTAGTCCTT 6720

Qy  6721 craaatcgaagagctttagactygctaaccgctgaragagggggaaccctgtttattttta 6780
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Qy  6841 attcsagatcgaatacaacgtakagcagargagcttcgaaacactggaaccctgggcctc 6900
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Qy  6901 ctcagccratggatgcccctggattctcccccttcttaggacctcagcagctataatattg 6960
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Db  6901 CTCACCRAYGGATGCCCCTGGATTCTCCCCTTTCTTAGGACCTCTTACCCAGCTATAAITTAITTG 6960

Qy  6961 ctactcctttggaccctgtatctttracctcctcttgttaactttgtcttcttcccagaatc 7020
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Db  6961 CTACYCCTCYTTGGACCCTGTATCTTTRACCTCCTTGTTAACTTTGTCTTCTTCCCAGRAATC 7020

Qy  7021 gaagctgtaaactacacaaatggagcccaagatgtccaagacatcacgcagaga 7080
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Db  7081 CCCTGGACCGGCGTTGYTAGCCCAGATCTGAITGTTAATGACATCAAAAGGCACCCCTCCT 7140

Qy  7141 gaggaaatctcagctgcacaacctctactacgccccaattcaggagaagagttagagc 7200
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Qy  7201 ggtsgtcggccaacctccccaacaggcaactcaggttttcctgttgaagatggggggactgaga 7260
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Db  7201 GGTSGTCGGCCAACCTCCCCAACAGCACACTCTAGGTTTTCCTGTTGAGATGGGGGGGACTGAGA 7260

Qy  7261 gacaggaactagctgaatttcctaggctgataaagaatccytaagcctags 7320
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Db  7261 GACAGGACTAGCTGGATTTCCTAGGCTGATATAAGAAIICCTTTAAGCTTAAGANTTCTAGCTGGATNGGGGGACTGAGA 7320

Qy  7321 accacatccaccttaaacacggggcttgcaacttagvtcacacctgaccaatcagcagag 7380
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Db  7321 ACCACATCCACCTTTAAGACAIIGGGGGCTTGCAACTTAGNANCCTTAAGCTGGYTCAGGAGAGAAGGTG 7380
```

RESULT 3

LOCUS   HSAC000064   56093 bp   DNA   PRI   13-NOV-1996
DEFINITION Human BAC clone RG083M05 from 7q21-7q22, complete sequence.
ACCESSION   AC000064
VERSION   AC000064.1   GI:1669369
KEYWORDS   HTG.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 56093)
  AUTHORS   Pauley,A.
  TITLE   The sequence of H. sapiens BAC clone RG083M05
  JOURNAL   Unpublished (1996)
REFERENCE   2 (bases 1 to 56093)
  AUTHORS   Waterston,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (13-NOV-1996)
            Genome Sequencing Center
            Department of Genetics, Washington University
            St. Louis, MO 63108, USA
COMMENT   e-mail: saplens@watson.wustl.edu

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
sections once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double-stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone; and the assembly was
confirmed by restriction digest.

SOURCE INFORMATION:
This clone is from the first release of the human BAC library. The
library contains cloned DNA from a human male fibroblast cell line
978SK. For references see: Shizuya et al., Proc. Natl. Acad. Sci.
89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
VECTOR: pBELO
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The orientation of this clone is unknown. Actual start of this
clone is at base position 1 of H_RG083M05; actual end is at 56093
of H_RG083M05.

This clone contains STS sWSS1725.

FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"

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                      complement(838..1131)
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     CDS             join(<1360,1503,4181,4370,4587,4774,6422,6556,
                      943,9547,11631,11773,11864,12021,13131,13296,
                      14885,14988,16349,16546,16837,16971)
                      /gene="WUGSC:H_RG083M05.1"
                      /note="ATPase; strong similarity to peroxisome
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                      /protein_id="AAB46346.1"
                      /db_xref="GI:1669371"
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                      SROSISTREKVLVITLDFOKALRGFLPASLRSVNLHKPRDLGWDKIGILHEVRDIILMD
                      TIQLPAKVCLKKEKYPELFANLPIRORTGILLYGPPGTGKTLLAGVIARESRMNFISV
                      KGPELLSKYIGASEOAVRDIFIRAQAAKPCILFFDEFESIAPRRGHDNTGVTDRVNQ
                      LLTOLDGVEGLQGVYVLAATSRPDLIDPALLRPGRLDKCVYCPPPDQVTISYLESKTQ
                      OMLHSFLVSRLEILNVLSDSLPLADDVDLQHVASVTDSFTGADLKALLYNAQLEALHG
                      NLLSKMSEILPDESKFNMYRLYFGGSSYESELGNGTRSSSDLSSQCLLSAPSSMTQDLPGVP
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     repeat_region   complement(6581..7133)
                      /rpt_family="Li"
     repeat_region   complement(7767..8037)
                      /rpt_family="ALU"
     repeat_region   complement(8186..8472)
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     misc_feature    8473..8625
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                      /note="match to human 3' EST H75782 (NID:g1049794), bases
                      287-444"
     repeat_region   8841..9161
                      /rpt_family="Li"
     misc_feature    9481..9547
                      /gene="WUGSC:H_RG083M05.1"
                      /note="match to human 5' EST H75921 (NID:g1050050), bases
                      21-348"
     misc_feature    complement(12612..12907)
                      /gene="WUGSC:H_RG083M05.1"
                      /note="match to human 5' EST N22627 (NID:g1130501), bases
                      276-343"
     repeat_region   complement(13670..13793)
                      /rpt_family="ALU"
     misc_feature    /gene="WUGSC:H_RG083M05.1"
                      /note="match to human 5' EST H41382 (NID:g917434), bases
                      143-266"
     repeat_region   13794..13877
                      /rpt_family="ALU"
     misc_feature    13878..13906
                      /gene="WUGSC:H_RG083M05.1"
                      /note="match to human 5' EST H41382 (NID:g917434), bases
                      30-58"
     repeat_region   13907..14104
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     repeat_region   complement(14110..14137)
                      /rpt_family="Li"
     repeat_region   complement(15618..15907)
                      /rpt_family="ALU"
     repeat_region   17227..17522
                      /rpt_family="ALU"
     repeat_region   18667..19235
     feature         /rpt_family="ALU"
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                      /rpt_family="ALU"
                      /note="similarity to various SS-RNA virus polyproteins;
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                      multiple human ESTs, see R68740 (NID:g842257)"
     exon            37316..37489
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                      /note="Grail prediction, score = 80"
                      /evidence=not_experimental
     repeat_region   complement(38938..39224)
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     misc_feature    39225..39707
                      /gene="WUGSC:H_RG083M05.1"
                      /note="match to multiple human ESTs, see N30113
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                      /rpt_family="ALU"
                      /note="match to multiple human ESTs, see N81064
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                      (NID:g273146)"
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     misc_feature    complement(47365..47782)
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                      /note="match to multiple human ESTs, see W37495
                      (NID:g1319089)"
     repeat_region   47898..48115
                      /rpt_family="ALU"
     misc_feature    /note="match to human 5' EST H62306 (NID:g1015138), bases
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     repeat_region   complement(48116..48405)
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     misc_feature    complement(48406..48584)
                      /rpt_family="ALU"
                      /note="match to human 3' EST N29952 (NID:g1148472), bases
                      290-455, and 5' EST R12730 (NID:g9765806)"
     repeat_region   complement(48787..49405)
                      /rpt_family="ALU"
     misc_feature    complement(49406..49534)
                      /gene="WUGSC:H_RG083M05.2"
                      /note="match to human 3' EST R65794 (NID:g9838432), bases
                      309-440"
     repeat_region   complement(49638..49672)
                      /rpt_family="ALU"
     misc_feature    complement(49674..49890)
                      /note="match to human 3' EST N29952 (NID:g1148472) and 5'
                      EST N29938 (NID:g1148458), sequences are from opposite
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     gene            complement(49698..51806)
                      /gene="WUGSC:H_RG083M05.2"
     CDS             complement(join(49698..49888,51575..51806))
                      /gene="WUGSC:H_RG083M05.2"
                      /note="coded for by human cDNAS W37389 (NID:g1319205),
                      R65891 (NID:g838529), R65794 (NID:g9838432) and R65794
                      (NID:g838432)"
                      /codon_start=1
                      /protein_id="AAB46345.1"
                      /db_xref="GI:1669370"
                      /translation="MFYFYFQCGIICFPOGVYYQIGDVVSVIDEQGKPYYAQIRGF
                      IQDQYCEKSAALTWLIPTLSSPRDQFDPASYIIGPEEDLPRKMEYLEPVCHAPSEYFK
                      SRSSPFPVTRPEKGYIWTHVGPTPAITIKESVANHL"
     exon            complement(51576..51758)
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                      /note="Grail prediction, score = 86"
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Query Match   85.0%;  Score 6448;  DB 93;  Length 56093;
Best Local Similarity 95.7%;  Pred. No. 0;
Matches 6681;  Conservative 195;  Mismatches 50;  Indels 53;  Gaps 27;

Qy    606 gatgggaaacgttcccgcaagacacaaaacgcccctaagacgtactctggaraattggga 665
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Qy    666 mcaatttgaccctccagaacacactaggaagaaaacgacttatcttctgcagtgccgcctg 725
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Qy    726 gcaactcctgagggaagtataaattataccacacaatcattacaagctagacytcttttgtagaa 785
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Qy    786 aaggcaaatgvagtgaagtgccataagtacaaacttctcttaggagacaactcac 845
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Db  31133 AAGGCAAATGGACTGAAGTGCCATAAGTACAAACTTTCTTTTTCATTAGGAGACAACTCAC 31192

Qy    846 aattatgtaaaaagtgtgattttatgctcccacagggaagccttcagagttctacctccctatc 905
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Qy    906 ccagcaatcccccgactcctccttcccamytaatacagaaycttcagaagttcactctccctatc 965
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Qy   1026 ccctccaagcagtgggaggaagaattcggcccagccagccaatggcatgtgcctttttyc 1085
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Qy   1086 tctcccagacttaaagcaaaatacagagactaggtaaattctcagatayctgatgg 1145
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Qy   1146 ctatatgrtgtttacaaggvgttaggaacaattcttcttgatctgacatggagagtatata 1205
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Qy   1206 tgtcactgctaaatcagacactaaaccccaaatgagagagaagtgccacataactgcagcct 1265
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Qy   1266 gagrgttggcgaatctctggtatctcagtcaatggatanggatgaacaacagaagg 1325
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Db  31611 GAGAGGTTTGGCGAATCTCTGGTATCTCAGTCAATGG---ATAGGATGACAACAG-AGG 31667

Qy   1326 aaaganaatgatctcccacacaggccagcargcagtcagttctasaccctcattggggac 1385
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Db  31668 AAAGAGAATGATTCCCCACACAGGCCAGCAGTCAGTTCCTCTAGACCCTCAATTGGG--- 31724

Qy   1386 acagaaaatcagtaacatgggaagagattgtgctcagagaacattgtgtgctaaagca 1445
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Db  31725 ACACAGAATCAGAACAT-GGAGATGGTTCCTCGAGACATTGCTAACTTGTGTGGCTAGAA 31783

Qy   1446 ggactaaggaaaactaagggaaaatctcaygaattactcaatgtgtccaccataacaca 1505
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Db  31784 GGACTAAGGAAAAACTAGGAGG-AAGTCTATGAATTACTCAAGATGTCCACCATAACACA 31842

Qy   1506 ggggaaggggaagaaaatcctactgcctttctggagagactaaggvaaggscattggaggaagc 1565
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Qy   1566 gtgcctctgtcaacctgactcttctgaaggccaactaatcttaaacgtaagtgtttatca 1625
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Db  31902 GTGCCTCTCTGTGTCAACCTGACTCTTCTGAAGGCCAACTAATCTTAAACGTAAGTTTATCA 31961
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Qy   1626 ctcagtcagctgcagacattag-taaaaacttcaaaagtctgccgtaggccgggaggcaaa 1684
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Db  31962 CTCAGTCAGCTGCAGACATTAGTAAAAACTTCAAAAGTCTGCCGGTAGGCCGGGAGGCAA 32021

Qy   1685 acttagaaaaccctattgaactttgcaacyctcggttcttttatataggagatcagaggggc 1744
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Db  32022 ACTTAGAAAACCCTATTGAACTTTGCAACCTTCGGTTTTTTATATAGGAGATCAGAGGAGC 32081

Qy   1745 aggcggaacacaggggacaaacgggattaaaaaacggaattaaaaaaaaaggccacacgcttagt 1804
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Db  32082 AGGGGGAACACAGGGGACAAACGGGATTAAAAAAACGGAATTAAAAAAAAAGGCCACGCCGCTTAGT 32141

Qy   1805 caagtggactttggaggctctcttggaagaagggaaaagctgggcaaagctaatgccaatagg 1864
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Qy   1985 ggacaaaggtctttgagtcagaagcaactaaccagatgatccggaagcagacgtcaggagg 2044
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This page contains a nucleotide sequence alignment (query "Qy" versus database "Db") arranged in two columns, with each aligned block showing a start coordinate, the sequence with match/mismatch bars (|, :, .), and an end coordinate.

Left column alignment blocks (start – end coordinates):

Row	Start	End
Db	32968	33025
Qy	2705	2764
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Qy	2765	2824
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Qy	2825	2884
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Qy	2885	2944
Db	33206	33265
Qy	2945	3004
Db	33266	33323
Qy	3005	3064
Db	33324	33383
Qy	3065	3124
Db	33384	33443
Qy	3125	3184
Db	33444	33499
Qy	3185	3244
Db	33500	33559
Qy	3245	3304
Db	33560	33618
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Qy	65	3424
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Qy	3425	3484
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Qy	3545	3604
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Qy	3605	3664
Db	33904	33963
Qy	3665	3724
Db	33964	34023
Qy	3725	3784
Db	34024	34083

Right column alignment blocks (start – end coordinates):

Row	Start	End
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Qy	4145	4204
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Db	34563	34622
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DEFINITION    Homo sapiens clone CTB-10G5, complete sequence.
ACCESSION     AC007566
VERSION       AC007566.2      GI:11181861
KEYWORDS      HTG.
SOURCE        human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 149194)
AUTHORS       Waterston,R.H.
TITLE         The sequence of Homo sapiens clone
JOURNAL       Unpublished
REFERENCE     2  (bases 1 to 149194)
AUTHORS       Waterston,R.H.
TITLE         Direct Submission
JOURNAL       Submitted (15-MAY-1999) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE     3  (bases 1 to 149194)
AUTHORS       Waterston,R.
TITLE         Direct Submission
JOURNAL       Submitted (02-OCT-2000) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE     4  (bases 1 to 149194)
AUTHORS       Waterston,R.H.
TITLE         Direct Submission
JOURNAL       Submitted (16-NOV-2000) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              63108, USA
              16, 2000 this sequence version replaced gi:4835815.
              ject name: H_RG010G05.
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                     /db_xref="taxon:9606"
                     /clone="CTB-10G5"
BASE COUNT     45439 a   29540 c   31229 g   42986 t
ORIGIN

Query Match    85.0%;   Score 6448;   DB 86;   Length 149194;
Best Local Similarity 95.7%;   Pred. No. 0;
Matches 6681;   Conservative 195;   Mismatches 50;   Indels 53;   Gaps 27;
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Db     37382 CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAAGGCACCCCCTCCTGAG 37381

Qy      7144 gaaatctcagtcgcacaacctctactacgccccaaattcagcaggaagcagttagagcggt 7203
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Db     37442 GAAATCTCAGTCGCACAACCTCTACTACGCCCCAAATTCAGCAGGAAGCAGTTAGAGCGGT 37441

Qy      7204 sgtcggccaacctcccaaacagcacttaggttttcctgttgagatggggsgactgagagac 7263
             :|||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
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Qy      7264 aggactagctggattcctagggctgaytaagaatccytaagcctagstgggaagtgacc 7323
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Qy      7324 acatccacccttaaacacggggcttgcaacttagYtcacacctgacatagagaagctc 7383
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Db     90871 AAGGCAAATGGAGTGAAGTGCCATAAGTACAAAACTTCTTTTCATTAAGAGAAGACAACTCAC 90872

Qy       846 aattatgtaaaaagtgtgattttatgccctacacaggaaagccttcagagttctacctcctatc 905
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Qy       966 aaggagatagacaaaaggggtaaacagtgaaccaaagtgtgccaatattccccaattatga 1025
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Db     90691 AAGGAGATAGACAAAAGGGGTTAAACAGTGAACCAAAGAGTGCCAATATTCCCCAATTATGA 90692

Qy      1026 ccccctcccaagcagtgggaggagagaattccggccccagccagagtgtcatgtgcyttttyy 1085
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Attachment: Search Report #2 09/446,024 Attach to Paper #14 Page 1 File Copy

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2001, 11:11:46 ; Search time 285.92 Seconds
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Title: US-09-446-024-11
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Scoring table: IDENTITY_NDC
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Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1415.8	18.7	2391	3	US-08-691-563C-57	Sequence 57, Appl
2	1069.4	14.1	1577	3	US-08-691-563C-89	Sequence 89, Appl
3	947.8	12.5	1167	3	US-08-691-563C-61	Sequence 61, Appl
4	932.4	12.3	1158	1	US-08-471-724-1	Sequence 1, Appl
5	932.4	12.3	1158	1	US-08-471-969-1	Sequence 1, Appl
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7	932.4	12.3	1158	2	US-08-470-006A-1	Sequence 1, Appl
8	932.4	12.3	1158	3	US-08-691-563C-1	Sequence 1, Appl
9	932.4	12.3	1158	4	US-09-200-990-1	Sequence 1, Appl
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11	624.4	8.2	2389	3	US-08-691-563C-52	Sequence 52, Appl
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42	319	4.2	495	3	US-08-691-563C-59	Sequence 59, Appl
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44	305.8	4.0	374	1	US-08-686-878A-47	Sequence 47, Appl
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ALIGNMENTS

RESULT 1
US-08-691-563C-57
Sequence 57, Application US/0869156363C
Patent No. 6001987
GENERAL INFORMATION:
; APPLICANT: Herve PERRON
; APPLICANT: Frederic BESEME
; APPLICANT: Frederic BEDIN
; APPLICANT: Glaucia PARANHOS-BACCALA
; APPLICANT: Florence KOMURIAN-PRADEL
; APPLICANT: Colette JOLIVET
; APPLICANT: Bernard MANDRAND
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
; TITLE OF INVENTION: THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,563C
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2391 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-691-563C-57

Query Match   18.7%; Score 1415.8; DB 3; Length 2391;
Best Local Similarity   78.4%; Pred. No. 0;

Matches 1817; Conservative 109; Mismatches 267; Indels 126; Gaps 19;

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Qy    2021 atgatccagcagcaggactgaggggtgcctggggcaaggcgccatccatgccatcaccctc 2080
           |||||||||||||||||||||||||||| |||| ||| ||||:|:|||| || ||||||| |
Db       1 ATGATCCAGCAGCAGGACNGAGGGGTGCCCGGGGCCAGCCGCCAGCCACCCTC 60

Qy    2081 acagagcgccctgggtatgctgaccattgagcaggccaggaaggt---tgtctcctggacact 2137
           ||||| |||||||||||||||||||||||||||||||||||||  |||:||||||||
Db      61 ACAGAGCCCCAGGGTATGCTCTTGACCATTGAGGGTCTCAGAAGGGTNACTGTCTCCTTGGACACT 120

Qy    2138 ggtgcggtcttcttagtctttctgtgtcccggacaactgtcctccagatcttgtcact 2197
           ||||:||||||||| |||||||||||||||||||||||:||||||||||||||||||
Db     121 GGCGGGNCCCTTCTCAGTCTTTACTTTCTGTGTCCTGGACAAACTGTGTCCTCAGACTGTGTCACT 180

Qy    2198 atttgagggggtccntaagacgggcagtcactagatactttycccaggccactaagtta 2257
           |||||||  |  ||||||||| |||||||||||||||:  ||||||||||||||||||
Db     181 GTCC---GAGGGGTCCTAGGACAGGCCAGTCACTAGATAC-TYCTCCAGCACTAAGTTG 236

Qy    2258 tgaactgggggagcttattattctttctaaattgtctgaaagccccacta 2317
           |||||||||||||||||||||||||||||||||:| || |||||||||||
Db     237 TG-ACTGGGGAAGACTTTACTGTTCTTCCCACATGCTCACTAGATAC-TYCTCCAGCACTAAGCTC 295

Qy    2318 ccttgttagggagagacattctagtcaaaagcagggggccattatacacctgaacataggag 2377
           ||||||||||||||||||| || ||||||||||||||||||||| ||| |||||||:|||||
Db     296 TCTTTGTTGGGGAGAGACATTCTAGCAAAAGCAGGGGCCATTATACTGTGAAATAGTAGGAG 355

Qy    2378 aaggaacacccgtttgttgttcncccctgcttgaggagaggaattaatcctgaagtctgtggca 2437
           ||||||||||||||||||||||:|||||||||||||||||||||||||||||||:|||||||||
Db     356 AAGGAACAACTGTTGTTGTTGT-CCCTGCTTGAGGAGAAGGAATTAATCCTGAAGTCCGGGCA 414

Qy    2438 acagaaggacaatatggacgagccaaaagcaggyatggactcetgttcaagttaaactaaagga 2497
           ||||||||||||| || ||||||||||||||||| ||||||||:|||||||||||||||||||
Db     415 ACAGAAGGACAATATGGACAAG-CAAAGAAATGCCCGCTCCTTGTTCAAGTTAAACTAAAGGA 473

Qy    2498 ttccacttccttctccctaccaaaggcagtacccctcagacacccaaacaaggatt 2557
           |||||||||:|||||||||||||||||||||||||||||||||||:| | | ||||||
Db     474 TTCCACCTCCTTTCCCTACCAAAGGCAGTACCCCTCAGACCCCAACCAACAAGAAACT 533

Qy    2558 ccaaaagattgttaaggacttaagcccaagggctagtacaaaccafgcataactccctg 2617
           ||||||||||||||||||||| ||||||||||:||||||||| ||||:||||||||||
Db     534 CCAAAAGATTGTAAAGGACCTAAAAGCCCAGGTAAAAACCGAAATAGCCCTTG 593

Qy    2618 cagtaattccgtagtggattgagggacacagaaaaaccagtggacagtggaggggttagtg 2677
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     594 CAAGACTCC-----AATTTAGGAGTAAGGAAAACCAACGACAGTGGA--GGTTAGTG 645

Qy    2678 caagatctcaggattacaagtggagcggttgtccttttatacccagctgtacctagccc 2737
           ||||||||||||||||||||||||||||||||| |||||||:||||||||||||||||
Db     646 CAAGAACTCAGGATTATCAAT-GAGGCTGTTGTGTTCCCTCTATACCCAGCTGTACCTTAACCC 704

Qy    2738 ttatactgtgmyttcccaaaataccaagaggaagcaagagtcggttacacatccctgaacttma 2797
           ||| |:||| ||||||||||||:|||||||||||||||||||||||:|||:||||||||||| |
Db     705 TTATACAGTGCTTTCCCAAATACCAGAGAAGCAGAGTGGTTTTTACAGTCCTGGACTTAA 764

Qy    2798 ggatgcctcctctgcatccctgtacatcctgactcctcaattctcttgcctttgaaga 2857
           |||||||||||||| || |||||||||||:||||||||||||:|||||:||||||||
Db     765 GGATGCCTTTTTCTGCATCCCTGTACGTCTCAATTCTGTTTGCCTTTGAAGA 824

Qy    2858 tacttcaaaacccacaatctcaactggactttttacccaagggttcagggatag 2917
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Db     825 TCCTTTGAACCCAAACGTCTCAACTTGACTGGTTTTACCCCAAGGGTTCAGGGATAG 884

Qy    2918 yccccatctatttggccaagccaagagcattagccaaagacttgagycaartymtcataacctggacac 2977
           : ||||||||||| ||| ||||:|||:||||||:|||||||||||||| |||::|||||||
Db     885 CCCCCANCTANTTGGCCAGGCATTGAGTCAATTCTCATACCTGGACAC 944

Qy    2978 tcttgtccttcrgtaktggatgatttacttttrgcygcvyrttcagaaaacctggtgtgca 3037
           ||||||||| || ||||||||||||||| |||:|||:|| |||||||||||||||||||||
Db     945 TCTTGTCCTTCAGTACATGGATGATTTACTTTTAGTGCGGCCGGAAAAAACCTTGTGTGCCA 1004

Qy    3038 tcaagccacccaagcrctcttmaattccctcgyacctgtggctacawggttttcaaaacs 3097
           |||||| ||||||| :|||||||||||||||||||||:||||||||:|||||||:
Db    1005 TCAAGGCCACCCAAGAACTCTTAAACTTTCCTCGCTGGCTACAAGGTTTTCAAAACC 1064
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Qy    3098 arargctcarctctgctcacagcagcaggtaaatactattaggyrcttaarattatccaaggcac 3157
           |:|:|||||:||||||||||||||||||||||| || |||:||||||||||||:||||||||||
Db    1065 AAAGGCTGGGCTCTTGCCTGCCACAGGAGGATTAGATACTNAGGGCTAAAATTATCCCAAGGGCAC 1124

Qy    3158 carggcccttcagttgaggyaaytryratccacgcctatacttggcttatcctcatccyccaaaccct 3217
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Db    1125 CAGGGCCCTTCAGTTGAGGAACGTACCCAGCTGTACTTCTACTGGCTTATCCCCAAAACCCT 1184

Qy    3218 aaagcaaactaagrgrrttccttggcrtaayaggyttctgcgaawatggattccccaggt 3277
           ||||||||||||:|:||||||||||| ||||||||||:|||| |:|||||||||||||||
Db    1185 AAAGCAAACTAAGAGGTTCCTTGGCCATAAGAGGTTCTGCGGCATACTGGGATTCCCCAGGT 1243

Qy    3278 wtggcraaatagccaggyycattawatacastaattaaggaaactcagaagaaacccaataacc 3337
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Db    1244 ACASCCCAAPAGCCAGGACCATTATATACACTAAATTAANGGAAACTCAGAAGCAACCAATPACCT 1303

Qy    3338 atttartaagatggayamctgaagymraagtggctttccaggccccctaaaggaaggcctta 3397
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Db    1304 ATTTAGTAAGATGGDACACCT---ACAGAAGTGGCTTTCCAGGCCCCTAAAGGAAGGCCCT-- 1358

Qy    3398 aacccaagyccccagtgttaaggyttggccaacdrgggccaagactttsttyataayrtcaacag 3457
           |||||||||||||||||||||||:||||||||||||||||||||||||||::|||||:|||||
Db    1359 AACCCAAGCCCCAGTGTTCAGCTYTGGCCAACACAGGGGCCAAGACTTTCTTTYATAYRTCAACAG 1417

Qy    3458 aaaaaacagraaayagcctctrggagcctcaacagrtccracgggacaagattttcttatatactgtt 3517
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Db    1418 AAAAAAACAGGAATAGCCTCTRGGAGCCTCAACAGGTCCTACGGGACAAGTCAGGGYGATCTCGNGAC 1477

Qy    3518 tggcryacctgastaaggaaaytgaatgtagtggtcaaagggttgtycytcattgttayggg 3577
           |||||||||||||||||||:||||||||||||:|||||||||| |||||||||||:|||||
Db    1478 TGGTATAACCYGAGTAAGGAAAATTGAATGTAGTGGTCAAAGGGTTGGCTCAGTTTTANGGG 1537

Qy    3578 tagtggttgcagtagcagtyktagtacctgaagcagtyaaaaataattaccaggyragagatc 3637
           |||||||||||||:|||||||||||:||||||||||||||||||||||||||||||:||||
Db    1538 TAATGGNGGCCAGTAGCAGTGTCTNAGYTATCGANGTAAGTCGGGAAAGGGTTGGCCTCATNGGTTTTANGGG 1597

Qy    3638 ttactgtgtggacatctcagakgtgaayrgccatcactactcactgctaactacctggc 3697
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Db    1598 TTNCTGTGTGGACACTCTAGGYCATTGANCGCACTCACTGCTAAAGGCCAGTGTGCTTGGT 1657

Qy    3698 tgtcagacaacygtttacttaaattcagggtctcatcattgaagggccagtgctgcrac 3757
           ||||||||||:||||||||||||||||||:|||||:|||||||||||||||||||||||
Db    1658 TGTCAGACAACCATTTACTTAANTACAGGCTCTANTTACTTGAAGAGCCAGTGCTGNGAC 1717

Qy    3758 tgtgcaacttgtgcaactctaacccagycncaattcttccagacacaatgaagaaagatar 3817
           ||||| ||||||||||| ||||| |||:|:|||||||||||||:||||||||||||:||||
Db    1718 TGCCGCACTTGTGCAACTCTTAAACC 1742

Qy    3818 aayataactgtcaacaartaatttctcaaaacctatgccactcgagggggaccttytagarg 3877
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Db    1743 ------CAAACTTAYGCTGCCCCAGAAGGGATCTTTNNPAG 1776

Qy    3878 ttccyyttgactgatccygacctcaact--tgtatacttgatggagttcctttgtagaa 3934
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Db    1777 GTCCCCTTAGCCCAACCTCAACTATAATAANTAACAGAGAGTTCGGTTTYGTGGAGAA 1836

Qy    3935 aaaggacttcgaaaagygggtatgc---agtggtcagtgataatgyttagttgaaagt 3991
           |||||:|||||||||||| || |||:||||||||||||:||||||||||||||:||
Db    1837 AAGGGATTACAAAGGGNAGGATATNCCANTAGGTGTGTTAGTGATAAACAGTACTTGAAAGT 1896

Qy    3992 aatccccct---cacttccaggagactagtgyctyagyctrgcagaaacttaagcyt---cayt 4045
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Db    1897 AAGGCCTCTTCCCCCNGGACCAGGTGTTAGTGATAAACAGTACTTGACCCG 1956

Qy    4046 kgggcactagaattaggagagraaaaaagygyaaatatatatacacagactcrrartatgct 4105
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Db    1957 CGAGCCTTAGAACTTTGAAAGGAGAGGAGAAAATGTGTATACAGATAGCAAGTANGCT 2016

Qy    4106 yacctagtcntccatgcccatgmr----------gcaatatgs 4138
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Db    2017 TATCTAATCCGAAATGCCCANGTGTTGTTTATCTAATCCGAAANTGCCCANGTTGCCAATATGG 2076
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Qy    4139  aragaaaaggaaattccttaacttcygaygaygaaacacctatcaamacatcaggaagcattagg 4198
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Db    2077  AAAGAAAAGGGAGTTCCTTAACCTCYCGGGGAACCCCATTAAATACCACAAGTYAATCATG    2136

Qy    4199  arattattaytgycwgtacagaacctataragaaggtggmagtcttacacgtgcyggggtcat 4258
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Db    2137  GAGTYATTGCACAGTGCAAAAACTCAAGGAGGTGGAAGTCTTACACTGCCAAAGCCAT       2196

Qy    4259  cannaaggaaagraaagggaaatasaaagrgaaygtgccaa 4297
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Db    2197  CAGAAAAAGGGAGAAAGGGAGAAGACCAGACATAAGTGGCTA 2235
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RESULT 2
US-08-691-563C-89
; Sequence 89, Application US/0869156 3C
; Patent No. 6001987
; GENERAL INFORMATION:
; APPLICANT: Herve PERRON
; APPLICANT: Frederic BEDIN
; APPLICANT: Frederic BESEME
; APPLICANT: Glaucia PARANHOS-BACCALA
; APPLICANT: Florence KOMURIAN-PRADEL
; APPLICANT: Colette JOLIVET
; APPLICANT: Bernard MANDRAND
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
; TITLE OF INVENTION: THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,563C
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1577 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-691-563C-89

Query Match   14.1%;   Score 1069.4;   DB 3;   Length 1577;
Best Local Similarity   88.0%;   Pred. No. 0;
Matches 1288;   Conservative   39;   Mismatches 111;   Indels 26;   Gaps 15;

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Qy    1801  caggcaagtggacttggaggctctggaaaaagctgggcgaaattgaatccctaa 1860
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Db     137  CAGGCAAGTGGACACATTGGGAGGCTCTGGAAAAAGGAAAAGTTGGGCGAAATTGAAATGCCTAA 196

Qy    1861  tagggcttgcttccaagtgcyggttctacaaggggacacctttaaaaaaagattg 1920
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Db     197  TAGGGCTTGCTTCCAGTGCAGTTCTACAAGGACGCGCTTTAGAAAAAGATTGTGCCAAGTAGAAA 256

Qy    1921  taagccgcccccttcgtccatgccccttatttcaaggggaatcacttggaagg 1980
            |:|||||||||||  :||||||||||||| |||||||||||  |||||||||||
Db     257  TAAGCCGCCCC--TCGTCCCATGCCCCCTTATTGTCCAAGGGAGAATCACTGGAAGGGCTACTGCCC 315

Qy    1981  caggggacaaaggtcttttgagtcagaagccactaaccagatgatccagacaagactg 2040
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Db     316  CAGGGGACGAAAGGTCCTCTGAGTCAGAAGCCACTAACCGATGATCCAGACAGCAGGACTG 375

Qy    2041  aggggtgcctgggcaaagcccaatcccatgccatcacctcacaagacccctgggtatgctt 2100
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Db     376  AGGGTGCCCGGGCAAGTGCCAGACGCCATCACCTCA--CAGACCCCGGGTAYGTTT 433

Qy    2101  gaccattgaggggccaggaaggt--tgtctcctggacacttggtcggttcttagtctt 2157
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Db     434  GACCAATTGAGAGACCAGGAAGGTTAACGTCTCCTGGCACAGCCGGCCTTCTCAGTCTT 493

Qy    2158  actctctctgtccccggacacactgtccctccaagatctgtccctattctgaggggggtcctaag 2217
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Db     494  ACTTTCCTTGTCCCCGGACAAATGTCCTCCAGACAANTTCGTTCGCACAYATCC---GAGGGGTCCTAAG 550

Qy    2218  acgggcagtcactagatacttcttgtccagccactaagttatcgaactgggggagcttattc 2277
            ||:||||||||||||||:|  |||:|||||||||||||||||:||:||||||||||||||||
Db     551  ACAGCCAGTGCACTACATAC-TTCTCYCAGCCCACTAAGTTGTG-ACYGGGGAACTTYACTC 608

Qy    2278  ttttcacatgtcttttctaattatgcttgaaagcccactaacctcttgttaggggagacatt 2337
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Db     609  TTTTCACATGCGTTTTCTAATTATGCCTGAAAGCCCCACTCCCTTGTTAGGGAGACATT 668

Qy    2338  ctagcaaagcaggggcccaattatacacctgaacataggagagaggaacacccgtttggtt 2397
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Db     669  TTAGCAAAAGCAGGGGCCCATTAATACACCTGAACATAGGAGAGAGGAATACCCATTTGCTTGT 728

Qy    2398  ncccccgcttgaggggaagttaatccttgaaagtctgggcaacagagaaggaggacaaatatgacg 2457
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Db     729  -CCCCTGCTTGGAGGAAGTTAATCCTTGAAGTCTGGGCAAACAGAAGAGGAGGGACAANTATGGACA 787

Qy    2458  agccaagaatgccccgtcctgttcaagttaaactaaagatccactctttcccctacc 2517
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Db     788  AG-CAAAGAATGCCCCGTCCCGTCCTGTTCAAGTTAAACTAAAGGATTCTGCCTCCTTTCTTTCCCTACC 846

Qy    2518  aaaggcagtaccccccagacccaaggcccaacacaaggattccaaaagaattgttaaggact 2577
            ||||||||||||||||||||||||||||||||| ||||||:|||||||||||:||||||||
Db     847  AAAGGAAGTACCCTCTTAGACCCGAGGCCCCTACAACAGGACT-CAAAAGAYNTGTTAAGGACC 905

Qy    2578  taaaacccaaggcttagtaaaacatgcataactccgtcagtaattccgtagtggatt 2637
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Db     906  TAAAAACCCAAGGCCTAGTAAAACATGCAGTAGCCCCTGCAAATACTCC-----AATT 958

Qy    2638  gaggaggcacagaaacccagtggacaagtggaggggttagtgcaagatctcaggattatcaa 2697
            ||| |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db     959  TTAGGAGTAAGGAAAACCCAACGGACACAGTGGA--GGTTAGTGCAAAGAYNCAGGATTATTAA 1017

Qy    2698  tggaggccgttgtgtccttttatacccagtgtaccctctagccctatactgtgnyttcccaaa 2757
            |||||||||||||||||||||||||||||||||||||||||||| |||||||::||:|||||
Db    1018  T-GAGGCTGTGTTTTCCTCTATACCCACTGTATCCAGCCCTTATACTCTGCTTTCCCCTAA 1076

Qy    2758  taccagaggaaagcagagtggttgttacasatcctggaacttmaggatgccttctctgatcc 2817
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Db    1077  TACCCAGAGGAAGCAGAGTAGTTTVACAGTCCTGGACCTTYAAGGATGCCTTCTTTCTGCATCC 1136

Qy    2818  ctgtacatcctgacctcaatctctgttgcctttgaagatacttcaaaccaarcatctc 2877
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Db    1137  CTGTACAACCTGAATCCTCGAATTCTGTTGCTTTGAAGATACTTCAAACCAAATGCTTC 1196

Qy    2878  aactcaacctggactttttacccaaggggtacggatagyccccatcatatttggccagg 2937
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Db    1197  AATTCACCTGGACTGTTTACCCCAGGGGTTCGGGGATAGCCCCCAYCTAYTTGGCCAGG 1256

Qy    2938  cattagcccaagacttgagycarrtymtcatacctggacactcttgtccctcrgtakgtgg 2997
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Db    1257  CATTAGCCCAAGACTTGAGCCAATTCTCATACCTGGACACTCTTGTCCCTCYGGTAYG-GG 1314

Qy    2998  atgattacttttrgcydgcyrttcaagaaacttgtgccatacaagcaccaagctctct 3057
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Db    2998  atgattacttttrgcydgcyrttcaagaaacttgtgccatacaagcaccaagctctct 3057
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RESULT 3
US-08-691-563C-61
Sequence 61, Application US/08691563C
Patent No. 6001987
GENERAL INFORMATION:
APPLICANT: Herve PERRON
APPLICANT: Frederic BESEME
APPLICANT: Frederic BEDIN
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Florence KOMURIAN-PRADEL
APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTIC
TITLE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

Query Match   12.5%; Score 947.8; DB 3; Length 1167;
Best Local Similarity   86.4%; Pred. No. 2.7e-283;
Matches 1013; Conservative 77; Mismatches 73; Indels 10; Gaps 6;

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Db  1315 ATGATTTAATTTAGCCACCGGTTCCATCAAGCCAACCTTGTCGTCCCATCAAGCCAACCGTTCT 1374
Qy  3058 tmaattcctcgcyacctgtygctacawggtttccaaacsaratgtcarctctctgctcac 3117
Db  1375 TAAATTCCTCACTCCGTGTGGGCGTACACAGGTTTCCAAACCTCAGCTCTGCTCAC 1434
Qy  3118 agcaggttaaatacttaggrctaarrattatccaaaggcaccaarggcccctcagtgaggaay 3177
Db  1435 AGCAGGTTAAATACTTAGGGTTAAAAATTATCCAAAAGGCCACAGGGCCCTCGTGAGGAAT 1494
Qy  3178 ryatcgcaagcctatactgcttatcctcatcycaaacccctaaagcgaactgrgrrttcc 3237
Db  1495 GTATCCAACCTGTACTGGGCTTTATCTTCATCCCAAAACCCTAAAGCAACTAAGA-AGGTCC 1553
Qy  3238 ttggcrtaayaggyttctgccgaa 3261
Db  1554 TTGGCATAACAGGTTTCTGCCGAA 1577

Db     1 AAGGAAACTCAGAAAGCCAATACCCATTTAGTTAAGATTGGACACCAGAAAGCAGCT 60
Qy  3313 aaggaaactcagaaagccaataccccattrartaagatggayamctgaaagymraagtggct 3372
Qy  3373 ttccaggccctaaagaaaggccttaaaacccaagtccagtgttaagdyttgccaacrggc 3432
Db    61 TTCCAGGCCCTAAAGAAAAATCCCT--AACCCAAGCCCCAGTGTTAAGCTTGCCAACCGGGC 118
Qy  3433 aagacttttsttyatayrtcacagaaaaacacagtaaayagtcttrggagtccttaacag 3492
Db   119 AAGACTTTTCTTTATAIGTCACAG--AAAAACAGGAATAGCTTCTAGGAGTCCTTACACAG 176
Qy  3493 rtccragggaygagcttgcaaccyrtggcryacctgastaaggaaaytgatgtagtggca 3552
Db   177 GTCCCAGGGAACAAGCTTGCAACCTGTGGGCATACCTGAGTAAGGAAAAACTGATGTANTGGCA 236
Qy  3553 aagggtgrcytcattgtttayggggtagtggttggcagtagcagtytagtatctgaagca 3612
Db   237 AAGGGTTGGCCTCATTGTTTACAGGTAG--GGCAGCAGTAGCAGTCTTAGTTTCTGAAACA 295
Qy  3613 gttaaaatatacagggragagatcttactgtgtggtgacaatccatgakgtgaayrgcata 3672
Db   296 GTTAAAATAATACAGGGAGAGATCTTACTGTGTGGACAATCTCAIGATGTGAACGGCATA 355
Qy  3673 ctcaactgctaaaggagagacttgtgggctgtcagacacacygttcacttacttaggctcta 3732
Db   356 CTCACTGCTTAAAGGAGAGACTTGTGGGCTGTCAGACAACCATTTACTTAAATAGCAGGTTCTA 415
Qy  3733 ttacttgaaargccagtgcttctgcacttgtcaacttcaaaccaagycncatt 3792
Db   416 TTACTTGAAGTGCCAGTGCTTGCGACTGCACATTTGTGTGCAACTTCTTAACCCAGCCACATTT 475
Qy  3793 cttccagacaatgaagaaaagtataraayataactgtcaacaartaaattctcaaacctat 3852
Db   476 CTTCCAGACAATGAAGAAAAGATAGAANATAAACATTAACYGTCAACAAGTAAATTGCTCAAACCTAT 535
Qy  3853 gcaactgcaagggacctytaagrgttccyttgactgatccygacccttcaaacttgtatac 3912
Db   536 GCTGCTCGGAGGGACCTTCTAGAGGTTCCCTTGACTGAICCCGACC-TCAAACTTGTATAC 594
Qy  3913 tgatggaagttccttgtagaaaaagaaggggagtgatggcagtgcagtga 3972
Db   595 TGAIGGAAGTTCCTTGGCAGAAAAAAGGACTTTGAAAAGCGGGATGCAGTGAICAGTGA 654
Qy  3973 taatggaatayttgaaagtaatccctcactccaggaactagtgctyagctrgcaagaact 4032
Db   655 TAATGGAATACTTGAAAGTAATCGGCCTCACTCCAGGAACTAGTGCTCAGCTAGGCAGAACT 714
Qy  4033 aatagccytcaytkgggcactagaaattaggaagaagraaaaaggyaaatatataacaga 4092
Db   715 AATAGCCCTCACTTGGGCACTAGAATTAGGAGAAGGGTAAAATATATATTCAGA 774
Qy  4093 ctctrartatgctyacctagtcntccatgcggcaatatgsaragaaagggaatt 4152
Db   775 CTCTAAGTATGCTTACCCTAGTCCCTCCATGCCGCAATATGGGAGAGAGAGGAATT 834
Qy  4153 cctaacttcygagrgaacacctatcaamacatca-ggaagccaattaggararttataytgg 4211
Db   835 CCTAACTTCTGAGGGAACACCTATCAAACCATCAGGGAAGCCATTAGGAGATTATTAITTGG 894
Qy  4212 cwgtacagagaaacctaragaggtgmagtcttacacactgcyggggtcatcanaaaggaaagr 4271
Db   895 CTGTACAGAGAAACCTARAAGAGGTGGGCAIGGGTCATCAGAAGAGAGG 954
Qy  4272 aaagggaaatasaaagrgaaaytgccaagcakatattgaagcmaaaagagagctgcaaggcagg 4331
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Qy  4332 accctccattagaaatgctattaaacttccctagtatataggggtaatcccttccggggaa 4391
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Qy  4392 ccaagcccccagtacttcagcaggagagaaaacagaatgyggggaacttcacgagg---cagtttc 4448
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